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SEQUENCE LISTING

<110> Spiegelman, Bruce
Yoon, Cliff

<120> Methods and Compositions for Modulating Gluconeogenesis
Using PGC-1

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<151> 2001-02-05

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<170> PatentIn Ver. 2.0

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gaa tat cgc aga gag tat gag aag cga gag tct gag agg gcc aag caa 2080
 Glu Tyr Arg Arg Glu Tyr Glu Lys Arg Glu Ser Glu Arg Ala Lys Gln
 650 655 660

agg gag agg cag agg cag aag gca att gaa gag cgc cgt gtg att tat 2128
 Arg Glu Arg Gln Arg Gln Lys Ala Ile Glu Glu Arg Arg Val Ile Tyr
 665 670 675 680

gtc ggt aaa atc aga cct gac aca aca cgg aca gaa ctg agg gac cgt 2176
 Val Gly Lys Ile Arg Pro Asp Thr Thr Arg Thr Glu Leu Arg Asp Arg
 685 690 695

ttt gaa gtt ttt ggt gaa att gag gag tgc aca gta aat ctg cgg gat 2224
 Phe Glu Val Phe Gly Glu Ile Glu Glu Cys Thr Val Asn Leu Arg Asp
 700 705 710

gat gga gac agc tat ggt ttc att acc tac cgt tat acc tgt gat gct 2272
 Asp Gly Asp Ser Tyr Gly Phe Ile Thr Tyr Arg Tyr Thr Cys Asp Ala
 715 720 725

ttt gct gct ctt gaa aat gga tac act ttg cgc agg tca aac gaa act 2320
 Phe Ala Ala Leu Glu Asn Gly Tyr Thr Leu Arg Arg Ser Asn Glu Thr
 730 735 740

gac ttt gag ctg tac ttt tgt gga cgc aag caa ttt ttc aag tct aac 2368
 Asp Phe Glu Leu Tyr Phe Cys Gly Arg Lys Gln Phe Phe Lys Ser Asn
 745 750 755 760

tat gca gac cta gat tca aac tca gat gac ttt gac cct gct tcc acc 2416
 Tyr Ala Asp Leu Asp Ser Asn Ser Asp Asp Phe Asp Pro Ala Ser Thr
 765 770 775

aag agc aag tat gac tct ctg gat ttt gat agt tta ctg aaa gaa gct 2464
 Lys Ser Lys Tyr Asp Ser Leu Asp Phe Asp Ser Leu Leu Lys Glu Ala
 780 785 790

cag aga agc ttg cgc agg taacatgttc cctagctgag gatgacagag 2512
 Gln Arg Ser Leu Arg Arg
 795

ggatggcgaa tacctcatgg gacagcgcgt ccttccctaa agactattgc aagtcatact 2572

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gtggtgtgtg tgcttgggtt aggggaagta tgtgtgggta catgtgagga ctggggggcac 2872

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atatatatat aaattaaaaa aaaaaaaaaa a 3023

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 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 5
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 20 25 30
 Leu Pro Glu Leu Asp Leu Ser Glu Leu Asp Val Asn Asp Leu Asp Thr
 35 40 45
 Asp Ser Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile
 50 55 60
 Ile Ser Asn Gln Tyr Asn Asn Glu Pro Ser Asn Ile Phe Glu Lys Ile
 65 70 75 80
 Asp Glu Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu
 85 90 95
 Asp Ser Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu
 100 105 110
 Thr Asp Gly Asp Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met
 115 120 125
 Pro Asp Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu
 130 135 140
 Lys Lys Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu
 145 150 155 160
 Cys Ser Gly Leu Ser Thr Gln Asn His Ala Asn His Asn His Arg Ile
 165 170 175
 Arg Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys
 180 185 190
 Ala Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser
 195 200 205
 Glu Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys
 210 215 220
 Pro Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Thr Ser Lys Lys
 225 230 235 240
 Lys Ser His Thr Gln Ser Gln Ser Gln His Leu Gln Ala Lys Pro Thr
 245 250 255
 Thr Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly
 260 265 270
 Ser Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu
 275 280 285

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Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala
 290 295 300
 Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys
 305 310 315 320
 Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser
 325 330 335
 Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser
 340 345 350
 Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His
 355 360 365
 Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His
 370 375 380
 Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile
 385 390 395 400
 Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser
 405 410 415
 Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys
 420 425 430
 Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser
 435 440 445
 Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys
 450 455 460
 His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys
 465 470 475 480
 Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys
 485 490 495
 Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp
 500 505 510
 Asp Ser Glu Asp Lys Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr
 515 520 525
 Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn
 530 535 540
 Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln
 545 550 555 560
 Arg Pro Gln Arg Met Arg Ser Arg Ser Arg Ser Phe Ser Arg His Arg
 565 570 575
 Ser Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly
 580 585 590
 Ser Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr
 595 600 605

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Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser
610 615 620

Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr
625 630 635 640

Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys
645 650 655

Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala
660 665 670

Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr
675 680 685

Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu
690 695 700

Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile
705 710 715 720

Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr
725 730 735

Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly
740 745 750

Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser
755 760 765

Asp Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp
770 775 780

Phe Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg
785 790 795